

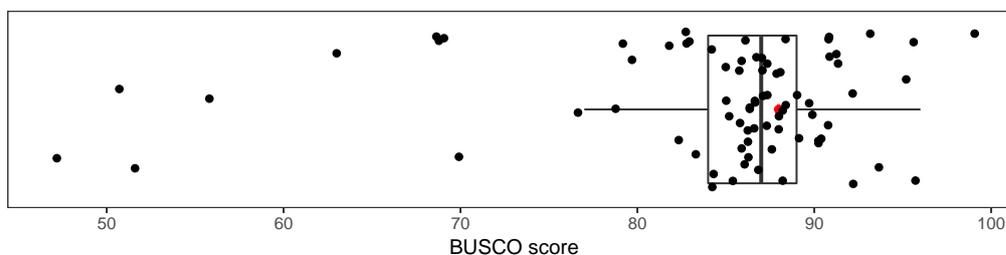
## Supplemental Information

**Table S1:** RTE1.Sar consensus sequence and copy information. The number of hits represent the number of reciprocal blastn hits to RTE1.Sar from Repbase Update. The consensus sequence was built with nhmmer software from a mafft alignment of the top 100 longest hit regions. ORFs were predicted with the ncbi ORF finder. The copy number was assessed with RepeatMasker and OneCodeToFindThemAll.

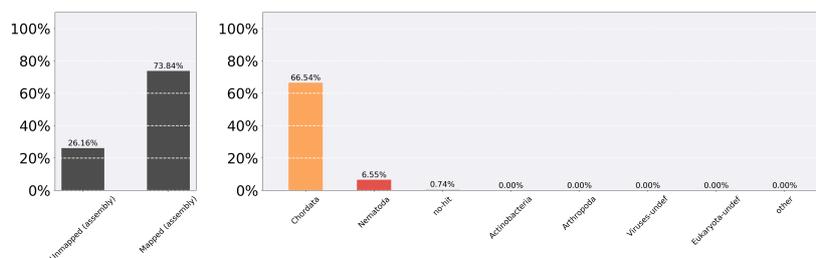
Species	accession	hits	consensus(bp)	ORF(aa)	copies
<i>Ancylostoma ceylanicum</i>	PRJNA231479	40	2662	893	784
<i>Angiostrongylus cantonensis</i>	PRJEB493	317	2356	793	14246
<i>Angiostrongylus costaricensis</i>	PRJEB494	155	2279	742	7784
<i>Haemonchus contortus</i>	PRJEB506	48	2790	838	3293
<i>Haemonchus placei</i>	PRJEB509	12	2502	267	1621
<i>Heligmosomoides polygyrus</i>	PRJEB1203	68	2520	838	9061
<i>Necator americanus</i>	PRJNA72135	27	1933	491	1989
<i>Nippostrongylus brasiliensis</i>	PRJEB511	56	2834	897	1483
<i>Teladorsagia circumcincta</i>	PRJNA72569	43	2834	927	1915
<i>Sorex araneus</i>	GCF_000181275.1	44098	3350	430	265858

**Table S2:** Completeness of *Sorex araneus* genome. BUSCO scores: C:88.1% [S:84.5%, D:3.6%], F:5.0%, M:6.9%, n:303. BUSCO scores are based on expected gene content from conserved genes.

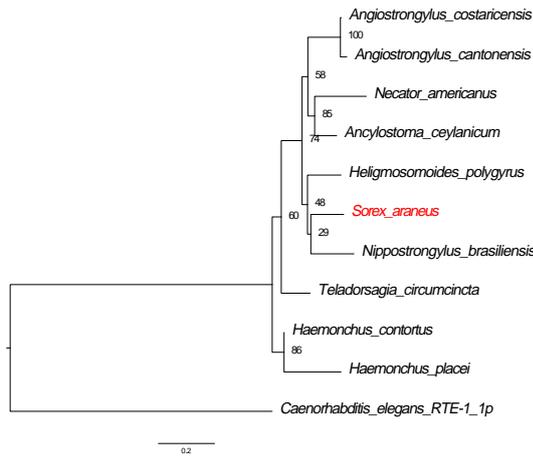
Category	n
Complete BUSCOs (C)	267
Complete and single-copy BUSCOs (S)	256
Complete and duplicated BUSCOs (D)	11
Fragmented BUSCOs (F)	15
Missing BUSCOs (M)	21
Total BUSCO groups searched	303



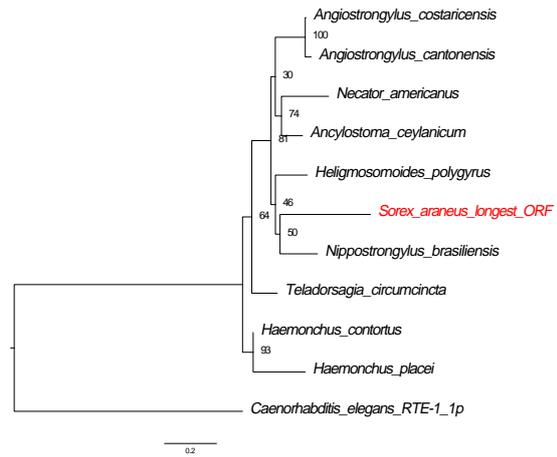
**Figure S1:** BUSCO scores for vertebrate Ensembl assemblies. Red dot: *S. araneus* assembly.



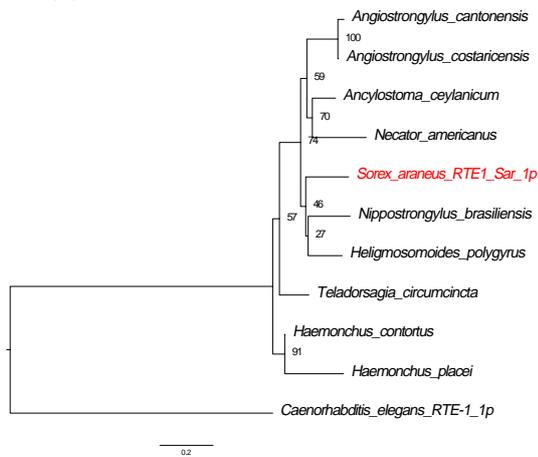
**Figure S2:** BlobTools analysis for contamination of *S. araneus* genome.



(a) *S. araneus* ORF from consensus sequence.

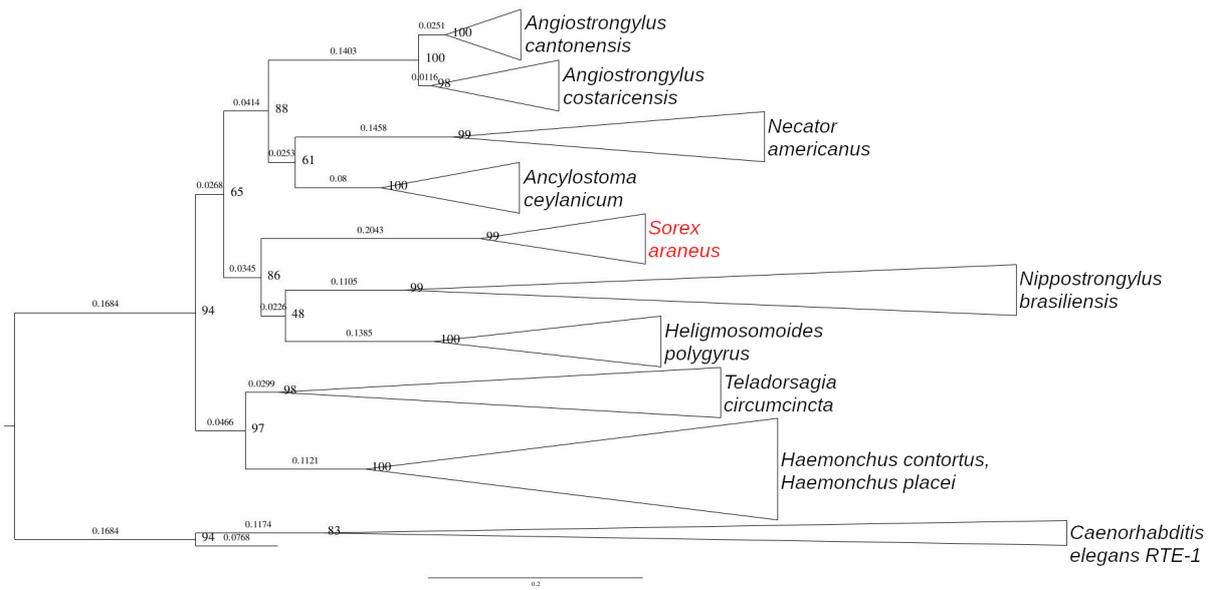


(b) *S. araneus* longest ORF from all individual copies.

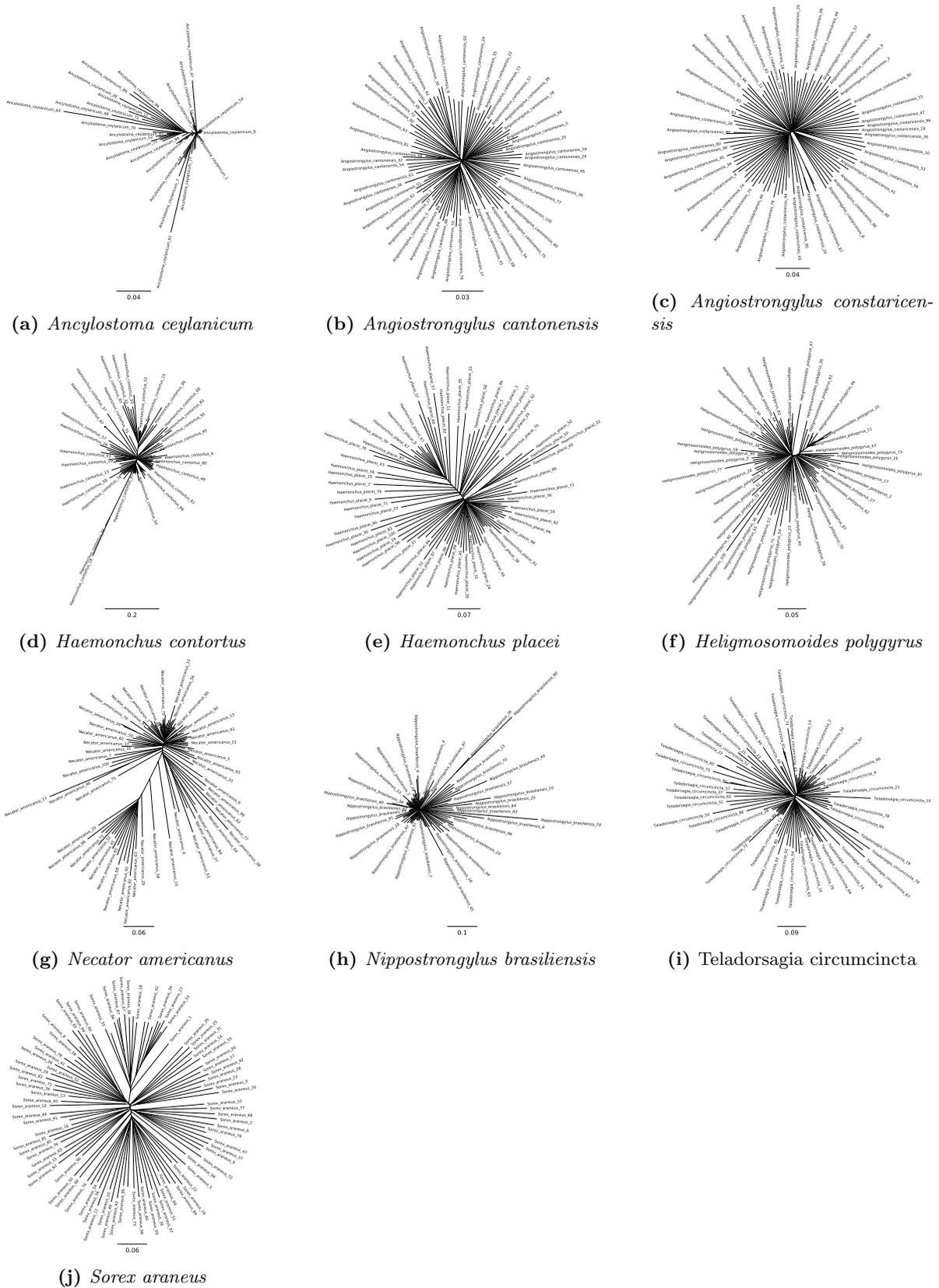


(c) *S. araneus* ORF from Replibase.

**Figure S3:** RAxML RTE1.Sar trees based on amino acids. Trees are based on ORFs predicted with NCBI's ORFfinder from their consensus sequences, with the ORF of RTE-1 of *C. elegans* from Replibase. We used different ORFs for *S. araneus*: 1) the consensus ORF, 2) the longest ORF from a copy, 3) the ORF from Replibase. The consensus ORF and the longest ORF of *S. araneus* are not full length. Support values are based on 1000 bootstrap replicates.



**Figure S4:** RAxML RTE1\_Sar tree based on individual copies. Copies were identified based on the species consensus sequence with RepeatMasker and OneCodeToFindThemAll. The 100 longest and least divergent copies were used for the phylogeny. The tree was rooted with RTE-1 copies of *C. elegans*. Support values are based on 1000 bootstrap replicates.



**Figure S5:** Phylogenies of species-specific RTE1\_Sar copies. Top 100 copies (length, % divergence) were aligned with mafft and phylogenies were built with RAxML GTRCAT. Star-like phylogenies indicate neutral evolution of RTE1\_Sar within species.